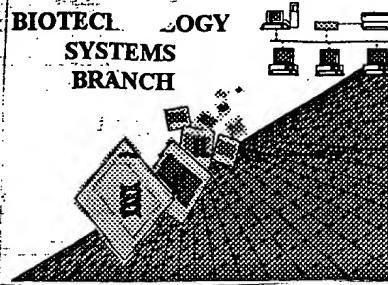


0400 12-28-00  
#112

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/728,420

Source: O1PE

Date Processed by STIC: 12/14/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED    SUGGESTED CORRECTION

SERIAL NUMBER: 09/728,420

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

|  |   |
|--|---|
| <input type="checkbox"/> 1      Wrapped Nucleic                            | <p>The number/text at the end of each line "wrapped" down to the next line.<br/>This may occur if your file was retrieved in a word processor after creating it.<br/>Please adjust your right margin to .3, as this will prevent "wrapping".</p>  |
| <input type="checkbox"/> 2      Wrapped Aminos                             | <p>The amino acid number/text at the end of each line "wrapped" down to the next line.<br/>This may occur if your file was retrieved in a word processor after creating it.<br/>Please adjust your right margin to .3, as this will prevent "wrapping".</p>   |
| <input type="checkbox"/> 3      Incorrect Line Length                      | <p>The rules require that a line not exceed 72 characters in length. This includes spaces.</p>  |
| <input type="checkbox"/> 4      Misaligned Amino Acid Numbering            | <p>The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.</p>  |
| <input type="checkbox"/> 5      Non-ASCII                                  | <p>This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.<br/>Please ensure your subsequent submission is saved in ASCII text so that it can be processed.</p>   |
| <input type="checkbox"/> 6      Variable Length                            | <p>Sequence(s) _____ contain n's or Xaa's which represented more than one residue.<br/>As per the rules, each n or Xaa can only represent a single residue.<br/>Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.</p>   |
| <input type="checkbox"/> 7      PatentIn ver. 2.0 "bug"                    | <p>A "bug" in PatentIn version 2.0 has caused the &lt;220&gt;-&lt;223&gt; section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant &lt;220&gt;-&lt;223&gt; section to the subsequent amino acid sequence. This applies primarily to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</p>                                   |
| <input type="checkbox"/> 8      Skipped Sequences (OLD RULES)              | <p>Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:<br/> <b>(2) INFORMATION FOR SEQ ID NO:X:</b><br/>           (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br/>           (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:<br/>           This sequence is intentionally skipped<br/><br/>           Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).         </p> |
| <input type="checkbox"/> 9      Skipped Sequences (NEW RULES)              | <p>Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.<br/> &lt;210&gt; sequence id number<br/> &lt;400&gt; sequence id number<br/> 000         </p>  |
| <input checked="" type="checkbox"/> 10     Use of n's or Xaa's (NEW RULES) | <p>Use of n's and/or Xaa's have been detected in the Sequence Listing.<br/>Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.<br/>In &lt;220&gt; to &lt;223&gt; section, please explain location of n or Xaa, and which residue n or Xaa represents.</p>   |
| <input type="checkbox"/> 11     Use of <213>Organism (NEW RULES)           | <p>Sequence(s) _____ are missing this mandatory field or its response.</p>  |
| <input type="checkbox"/> 12     Use of <220>Feature (NEW RULES)            | <p>Sequence(s) _____ are missing the &lt;220&gt;Feature and associated headings.<br/>Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if &lt;213&gt;ORGANISM is "Artificial" or "Unknown"<br/>Please explain source of genetic material in &lt;220&gt; to &lt;223&gt; section.<br/>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)</p>  |
| <input type="checkbox"/> 13     PatentIn ver. 2.0 "bug"                    | <p>Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.</p>   |

OIPE

Does Not Comply  
Corrected Diskette Needed

*4.5  
JPR*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/728,420

DATE: 12/14/2000  
TIME: 10:43:36

Input Set : A:\A-579-c.app  
Output Set: N:\CRF3\12142000\I728420.raw

3 <110> APPLICANT: Yoshinaga, Steven K.  
 5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES INVOLVED IN IMMUNE RESPONSE  
 7 <130> FILE REFERENCE: A-579-C  
**OK** 9 <140> CURRENT APPLICATION NUMBER: US/09/728,420  
 10 <141> CURRENT FILING DATE: 2000-11-28  
 12 <160> NUMBER OF SEQ ID NOS: 35  
 14 <170> SOFTWARE: PatentIn Ver. 2.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 600  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: mouse  
 21 <220> FEATURE:  
**OK** 22 <221> NAME/KEY: CDS  
**OK** 23 <222> LOCATION: Complement((1)..(600))  
 25 <400> SEQUENCE: 1  
 26 atg aag ccg tac ttc tgc cgt gtc ttt gtc ttc tgc tca atc aga 48  
 27 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg  
 28 1 5 10 15  
 30 ctt tta aca gga gaa atc aat ggc tcc gcc gat cat agg atg ttt tca 96  
 31 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser  
 32 20 25 30  
 34 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144  
 35 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val  
 36 35 40 45  
 38 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192  
 39 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
 40 50 55 60  
 42 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240  
 43 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
 44 65 70 75 80  
 46 atg ctc tgt cta tat cat ctg tca aac aac ugc gtc tct ttt ttc cta 288  
 47 Met Leu Cys Leu Tyr His Leu Ser Asn Ser Val Ser Phe Leu  
 48 85 90 95  
 50 aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc 336  
 51 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
 52 100 105 110  
 54 att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat 384  
 55 Ile Phe Asp Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr  
 56 115 120 125  
 58 ttg cat att tat gaa tcc cag ctc tgc cag ctg aag ctc tgg cta 432  
 59 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
 60 130 135 140  
 62 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata 480  
 63 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile  
 64 145 150 155 160  
 66 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac 528  
 67 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/728,420

DATE: 12/14/2000  
TIME: 10:43:36

Input Set : A:\A-579-c.app  
Output Set: N:\CRF3\12142000\I728420.raw

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68      165          170          175
70 cct eat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag  576
71 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
72          180          185          190
74 tct aga ctt gca ggt gtg acc tca
75 Ser Arg Leu Ala Gly Val Thr Ser
76          195          200
79 <210> SEQ ID NO: 2
80 <211> LENGTH: 200
81 <212> TYPE: PRT
82 <213> ORGANISM: mouse
84 <400> SEQUENCE: 2
85 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
86          1           5          10          15
88 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
89          20          25          30
91 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
92          35          40          45
94 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
95          50          55          60
97 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
98          65          70          75          80
100 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
101          85          90          95
103 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
104          100          105          110
106 Ile Phe Asp Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
107          115          120          125
109 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
110          130          135          140
112 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
113          145          150          155          160
115 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
116          165          170          175
118 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
119          180          185          190
121 Ser Arg Leu Ala Gly Val Thr Ser
122          195          200
126 <210> SEQ ID NO: 3
127 <211> LENGTH: 200
128 <212> TYPE: PRT
129 <213> ORGANISM: mouse
131 <400> SEQUENCE: 3
132 Met Lys Pro Tyr Phe Cys Arg Val Phe Val Phe Cys Phe Leu Ile Arg
133          1           5           10           15
135 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
136          20          25          30
138 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
139          35          40          45

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/728,420

DATE: 12/14/2000  
TIME: 10:43:36

Input Set : A:\A-579-c.app  
Output Set: N:\CRF3\12142000\I728420.raw

141 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu  
142 50 55 60  
144 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro  
145 65 70 75 80  
147 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu  
148 85 90 95  
150 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser  
151 100 105 110  
153 Ile Phe Asp Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr  
154 115 120 125  
156 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu  
157 130 135 140  
159 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Phe Gly Cys Ile  
160 145 150 155 160  
162 Leu Ile Ile Trp Phe Ser Lys Lys Tyr Gly Ser Ser Val His Asp  
163 165 170 175  
165 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys  
166 180 185 190  
168 Ser Arg Leu Ala Gly Val Thr Ser  
169 195 200  
172 <210> SEQ ID NO: 4  
173 <211> LENGTH: 218  
174 <212> TYPE: PRT  
175 <213> ORGANISM: mouse  
177 <400> SEQUENCE: 4  
178 Met Thr Leu Arg Leu Leu Phe Leu Ala Leu Asn Phe Phe Ser Val Gln  
179 1 5 10 15  
181 Val Thr Glu Asn Lys Ile Leu Val Lys Gln Ser Pro Leu Leu Val Val  
182 20 25 30  
184 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu  
185 35 40 45  
187 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val  
188 50 55 60  
190 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gin Pro Gln Phe Arg  
191 65 70 75 80  
193 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val  
194 85 90 95  
196 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe  
197 100 105 110  
199 Cys Lys Ile Glu Phe Met Tyr Pro Pro Tyr Leu Asp Asn Glu Arg  
200 115 120 125  
202 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr  
203 130 135 140  
205 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val  
206 145 150 155 160  
208 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp  
209 165 170 175  
211 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met  
212 180 185 190

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/728,420

DATE: 12/14/2000  
TIME: 10:43:36

Input Set : A:\A-579-c.app  
Output Set: N:\CRF3\12142000\I728420.raw

214 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala  
215 195 200 205

217 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro  
218 210 215

221 <210> SEQ ID NO: 5

222 <211> LENGTH: 234

223 <212> TYPE: PRT

224 <213> ORGANISM: Artificial Sequence

225 <220> FEATURE:

227 <223> OTHER INFORMATION: Description of Artificial Sequence Synthetic

228 Oligonucleotide

230 <400> SEQUENCE: 5

W--> 231 Met Xaa Arg  
232 1 5 10 15

W--> 234 Leu Leu Xaa  
235 20 25 30

W--> 237 Xaa  
238 35 40 45

W--> 240 Val Xaa Xaa Ser Cys Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
241 50 55 60

W--> 243 Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Cys Xaa  
244 65 70 75 80

W--> 246 Xaa  
247 85 90 95

W--> 249 Xaa Xaa Cys Xaa Xaa Xaa Xaa Asn Xaa Xaa Val Xaa Phe Xaa Leu  
250 100 105 110

W--> 252 Xaa Asn Xaa Xaa Xaa Xaa Xaa Xaa Tyr Phe Cys Xaa Xaa Xaa  
253 115 120 125

W--> 255 Xaa Xaa Xaa Pro Pro Pro Xaa Xaa Xaa Xaa Ser Xaa Gly Xaa  
256 130 140

W--> 258 Xaa Xaa His Ile Xaa Glu Xaa Xaa Leu Cys Xaa Xaa Xaa Xaa Xaa  
259 145 150 155 160

W--> 261 Lys Leu Xaa Trp Xaa Leu Xaa Val Xaa Xaa Xaa Xaa Phe Xaa Xaa  
262 165 170 175

W--> 264 Xaa Xaa Leu Leu Xaa Xaa Xaa Xaa Leu Xaa Xaa Ile Trp Xaa Xaa Xaa  
265 180 185 190

W--> 267 Xaa Pro Xaa  
268 195 200 205

W--> 270 Xaa Arg  
271 210 215 220

W--> 273 Xaa Xaa Ala Xaa Xaa Xaa Xaa Xaa Xaa  
274 225 230

277 <210> SEQ ID NO: 6

278 <211> LENGTH: 966

279 <212> TYPE: DNA

280 <213> ORGANISM: mouse

282 <220> FEATURE:

283 <221> NAME/KEY: CDS

W--> 284 <222> LOCATION: Complement((1)..(966))

This is an amino acid sequence.

see item 10  
in Err  
Summary Sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/728,420

DATE: 12/14/2000  
TIME: 10:43:36

Input Set : A:\A-579-c.app  
Output Set: N:\CRF3\12142000\I728420.raw

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286 <400> SEQUENCE: 6
287 atg cag cta aag tgt ccc tgt ttt gtg tcc ttg gga acc agg cag cct 48
288 Met Gln Leu Lys Cys Pro Cys Phe Val Ser Leu Gly Thr Arg Gln Pro
289    1           5          10          15
290    2           6          11          16
291 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt 96
292 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
293    3           8          13          18
294    4           9          14          19
295 ctg ttc ttg ctg ctg ttg agc agc ctc tct gct gcc tct gca gag act 144
296 Leu Phe Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
297    5           10          15          20
298    6           11          16          21
299 gaa gtc ggt gca atg gtg ggc agc aat gtc gtg ctc agc tyc att gac 192
300 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
301    7           12          17          22
302    8           13          18          23
303 ccc cac aca cgc cat ttc aac ttg agt ggt ctg tat gtc tat ttg caa 240
304 Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
305    9           14          19          24
306    10          15          20          25
307 atc gaa aac cca gaa gtt tcg gtg act tac tac ctg oct tac aag tct 288
308 Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
309    11          16          21          26
310    12          17          22          27
311 cca ggg atc aat gtc gac agt tcc tac aac aac agg ggc cat ctg tcc 336
312 Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
313    13          18          23          28
314    14          19          24          29
315 ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc 384
316 Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
317    15          20          25          30
318    16          21          26          31
319 acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca 432
320 Thr Pro Gln Asp Thr Gln Giv Phe Thr Cys Arg Val Phe Met Asn Thr
321    17          22          27          32
322    18          23          28          33
323 gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg 480
324 Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
325    19          24          29          34
326    20          25          30          35
327 qca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac 528
328 Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
329    21          26          31          36
330    22          27          32          37
331 ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca 576
332 Pro Gly Gin Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
333    23          28          33          38
334    24          29          34          39
335 gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac 624
336 Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
337    25          30          35          40
338    26          31          36          41
339 acq gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat 672
340 Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
341    27          32          37          42
342    28          33          38          43
343 gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt 720
344 Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
345    29          34          39          44
346    30          35          40          45
347 ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att 768
348 Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
349    31          36          41          46
            245          250          255

```

FYI:

**Please Note:**

**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.**

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/728,420

DATE: 12/14/2000

TIME: 10:43:37

Input Set : A:\A-579-c.app

Output Set: N:\CRF3\12142000\I728420.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:23 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:1, CDS LOCATION: Complement((1)..(600))  
L:231 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:231 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:231 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5  
L:234 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:234 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
M:340 Repeated in SeqNo=5  
L:237 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:237 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:240 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:240 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:243 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:243 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:246 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:246 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
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L:258 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:258 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:264 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:264 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
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L:267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:273 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5  
L:273 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5  
L:284 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:6, CDS LOCATION: Complement((1)..(966))  
L:589 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:589 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:589 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10  
L:592 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:592 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
M:340 Repeated in SeqNo=10  
L:595 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:595 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:598 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:598 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:601 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:601 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/728,420

DATE: 12/14/2000  
TIME: 10:43:37

Input Set : A:\A-579-c.app  
Output Set: N:\CRF3\12142000\I728420.raw

L:604 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:604 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:607 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:607 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:610 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:610 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:613 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:613 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:616 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10  
L:616 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10  
L:660 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:11, CDS LOCATION: Complement((1)..(864))  
L:927 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15  
M:340 Repeated in SeqNo=15  
L:1298 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:20  
M:340 Repeated in SeqNo=20